

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/995,542

DATE: 12/05/2001

TIME: 11:50:30

Input Set : A:\00658Aseq.txt

Output Set: N:\CRF3\11212001\I995542.raw

ENTERED

3 <110> APPLICANT: Shutter, John
 4 Ulias, Laarni
 6 <120> TITLE OF INVENTION: ATP-Binding Cassette Transporter-Like Molecules and
 7 Uses Thereof
 9 <130> FILE REFERENCE: 00-658-A
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/995,542
 C--> 12 <141> CURRENT FILING DATE: 2001-11-28
 14 <150> PRIOR APPLICATION NUMBER: 60/253,520
 15 <151> PRIOR FILING DATE: 2000-11-28
 17 <160> NUMBER OF SEQ ID NOS: 24
 19 <170> SOFTWARE: PatentIn Ver. 2.0
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 22 <211> LENGTH: 6633
 23 <212> TYPE: DNA
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 28 <222> LOCATION: (1)..(138)
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 32 <222> LOCATION: (1)..(6504)
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 37 1 5 10 15
 39 tat cga cgg aga caa ccg atc caa cta ctg gag ttg ctt tgg ccc 96
 40 Tyr Arg Arg Gln Pro Ile Gln Leu Leu Val Glu Leu Leu Trp Pro
 41 20 25 30
 43 ctc ttc ctc ttc ttc atc cta gtg gct gtc cgt cac tcc cac ccc cct 144
 44 Leu Phe Leu Phe Phe Ile Leu Val Ala Val Arg His Ser His Pro Pro
 45 35 40 45
 47 ctg gag cat cac gaa tgc cac ttt cca aac aag cca tta cca tcg gcg 192
 48 Leu Glu His His Glu Cys His Phe Pro Asn Lys Pro Leu Pro Ser Ala
 49 50 55 60
 51 ggc acg gtg ccc tgg ctg cag ggc ctt gtc tgc aac gta aac aac tcc 240
 52 Gly Thr Val Pro Trp Leu Gln Gly Leu Val Cys Asn Val Asn Asn Ser
 53 65 70 75 80
 55 tgc ttc cag cac cca acg cct ggc gag aag cct ggg gtc ctg agt aac 288
 56 Cys Phe Gln His Pro Thr Pro Gly Glu Lys Pro Gly Val Leu Ser Asn
 57 85 90 95
 59 ttt aag gat tcc ttg atc tcg agg ctc ctc gct gat acc cgc aca gtg 336
 60 Phe Lys Asp Ser Leu Ile Ser Arg Leu Leu Ala Asp Thr Arg Thr Val
 61 100 105 110
 63 ctc ggg ggc cac agc atc cag gac atg ctg gat gcc ctg ggg aaa ctg 384
 64 Leu Gly Gly His Ser Ile Gln Asp Met Leu Asp Ala Leu Gly Lys Leu
 65 115 120 125
 67 atc ccc gtg ctc agg gca gtt gga ggt gga gca cga cca cag gag agt 432

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72 Asp Gln Pro Thr Ser Gln Gly Ser Val Thr Lys Leu Leu Glu Lys Ile
73 145      150      155      160
75 ctg caa agg gca tcc ctg gat cct gtg ctg ggt caa gcc cag gat tct 528
76 Leu Gln Arg Ala Ser Leu Asp Pro Val Leu Gly Gln Ala Gln Asp Ser
77      165      170      175
79 atg aga aag ttc tca gat gct atc agg gat ctt gcc cag gag ctc ctg 576
80 Met Arg Lys Phe Ser Asp Ala Ile Arg Asp Leu Ala Gln Glu Leu Leu
81      180      185      190
83 aca ctg ccc agc ctg atg gag ctc cga gct ttg ctg cgg agg ccc cga 624
84 Thr Leu Pro Ser Leu Met Glu Leu Arg Ala Leu Leu Arg Arg Pro Arg
85      195      200      205
87 ggg tca gct ggt tct ctg gag ctg gtt tgc gag gcc ctc tgc agt acc 672
88 Gly Ser Ala Gly Ser Leu Glu Leu Val Ser Glu Ala Leu Cys Ser Thr
89      210      215      220
91 aag gga ccc agc agt cca ggg ggc ctg tcc ctc aat tgg tac gaa gcc 720
92 Lys Gly Pro Ser Ser Pro Gly Gly Leu Ser Leu Asn Trp Tyr Glu Ala
93 225      230      235      240
95 aac cag ctt aat gag ttc atg ggg cca gag gtg gcc cct gcc ctg cct 768
96 Asn Gln Leu Asn Glu Phe Met Gly Pro Glu Val Ala Pro Ala Leu Pro
97      245      250      255
99 gac aac agt ctc agc cct gcc tgc tct gag ttt gtg ggg aca ctg gat 816
100 Asp Asn Ser Leu Ser Pro Ala Cys Ser Glu Phe Val Gly Thr Leu Asp
101      260      265      270
103 gac cac cct gtg tct cgg ctg ctc tgg agg cgc ctg aag cca ttg atc 864
104 Asp His Pro Val Ser Arg Leu Leu Trp Arg Arg Leu Lys Pro Leu Ile
105      275      280      285
107 ctc ggg aaa att ctc ttt gca cct gac aca aac ttc act cgg aag ctc 912
108 Leu Gly Lys Ile Leu Phe Ala Pro Asp Thr Asn Phe Thr Arg Lys Leu
109      290      295      300
111 atg gct cag gtg aac cag acc ttc gag gag ctg gct ctg ttg agg gac 960
112 Met Ala Gln Val Asn Gln Thr Phe Glu Glu Leu Ala Leu Leu Arg Asp
113 305      310      315      320
115 cta cac gaa ctc tgg ggg gtg ctg gga ccc cag atc ttc aac ttc atg 1008
116 Leu His Glu Leu Trp Gly Val Leu Gly Pro Gln Ile Phe Asn Phe Met
117      325      330      335
119 aat gac agt acc aac gtg gcc atg ctt cag agg ctt ctg gat gtg ggg 1056
120 Asn Asp Ser Thr Asn Val Ala Met Leu Gln Arg Leu Leu Asp Val Gly
121      340      345      350
123 ggc aca ggg cag agg cag cag aca ccc aga gcc cag aag aag ttg gag 1104
124 Gly Thr Gly Gln Arg Gln Gln Thr Pro Arg Ala Gln Lys Lys Leu Glu
125      355      360      365
127 gct atc aaa gac ttt ctg gat cct agt agg ggt ggc tac agc tgg cgg 1152
128 Ala Ile Lys Asp Phe Leu Asp Pro Ser Arg Gly Gly Tyr Ser Trp Arg
129      370      375      380
131 gag gcc cac gca gat atg gga cgc ctg gct gga atc cta gga caa atg 1200
132 Glu Ala His Ala Asp Met Gly Arg Leu Ala Gly Ile Leu Gly Gln Met

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133	385		390		395		400	
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139	gct	ctt	gtg	tcc	cgt	gcc	ctg	gag
140	Ala	Leu	Val	Ser	Arg	Ala	Leu	Glu
141				420			425	
143	gca	ggc	atc	gtg	ttc	ctg	agc	cca
144	Ala	Gly	Ile	Val	Phe	Leu	Ser	Pro
145			435				440	
147	ctg	tca	tct	cca	gcc	ctg	agt	cct
148	Leu	Ser	Ser	Pro	Ala	Leu	Ser	Pro
149		450				455		460
151	atg	gat	atc	gat	gat	gtc	aca	agg
152	Met	Asp	Ile	Asp	Asp	Val	Thr	Arg
153	465				470		475	
155	tgg	gac	cca	ggg	ccg	tca	gca	gat
156	Trp	Asp	Pro	Gly	Pro	Ser	Ala	Asp
157				485			490	
159	tgg	gga	ggc	ttc	gtg	tac	ctg	cag
160	Trp	Gly	Gly	Phe	Val	Tyr	Leu	Gln
161			500				505	
163	cga	gtg	ctc	ggg	ggc	ggg	aac	tcc
164	Arg	Val	Leu	Gly	Gly	Gly	Asn	Ser
165		515					520	
167	atg	cca	cac	ccc	tgc	tac	gtg	gat
168	Met	Pro	His	Pro	Cys	Tyr	Val	Asp
169		530					535	
171	cgg	tct	ctg	cct	ctg	ttt	ctg	act
172	Arg	Ser	Leu	Pro	Leu	Phe	Leu	Thr
173	545				550		555	
175	ctc	act	gtg	aag	gcc	gtg	gtg	cgt
176	Leu	Thr	Val	Lys	Ala	Val	Val	Arg
177			565				570	
179	acc	atg	cgt	gcg	atg	ggg	ctg	agc
180	Thr	Met	Arg	Ala	Met	Gly	Leu	Ser
181			580				585	
183	ttc	ctc	agc	tgc	ctg	gga	ccc	ttc
184	Phe	Leu	Ser	Cys	Leu	Gly	Pro	Phe
185			595				600	
187	tta	gtg	ctt	aag	cta	ggg	aac	atc
188	Leu	Val	Leu	Lys	Leu	Gly	Asn	Ile
189		610					615	
191	atc	ttc	ctt	ttc	ttg	gcg	gcc	ttc
192	Ile	Phe	Leu	Phe	Leu	Ala	Ala	Phe
193	625				630		635	
195	ttt	ctg	ctc	agc	gcc	ttc	ttc	tcc
196	Phe	Leu	Leu	Ser	Ala	Phe	Phe	Ser
197			645				650	

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200	Gly Gly Leu Ala Tyr Phe Ala Leu Tyr Leu Pro Tyr Val Leu Cys Val	
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203	gcc tgg cgc gag cgc ctg cac ctg gcc gga ctc tta gct gcg agc ctg	2064
204	Ala Trp Arg Glu Arg Leu His Leu Gly Gly Leu Leu Ala Ala Ser Leu	
205	675 680 685	
207	ctg tcc cct gta gcc ttt gcc ttt gga tgc gaa agc ctg gcg cta cta	2112
208	Leu Ser Pro Val Ala Phe Gly Phe Gly Cys Glu Ser Leu Ala Leu Leu	
209	690 695 700	
211	gag gag cag gga gac ggg gct cag tgg cac aat ttg gcc aca gcc ccc	2160
212	Glu Glu Gln Gly Asp Gly Ala Gln Trp His Asn Leu Gly Thr Gly Pro	
213	705 710 715 720	
215	gcg gag gac gtc ttc agc ctg gcc cag gtg tct gcc ttc ctg ttg ctt	2208
216	Ala Glu Asp Val Phe Ser Leu Ala Gln Val Ser Ala Phe Leu Leu Leu	
217	725 730 735	
219	gat gcc gtc atc tac gcc ctt gcc ctc tgg tac cta gag gct gtg tgc	2256
220	Asp Ala Val Ile Tyr Gly Leu Ala Leu Trp Tyr Leu Glu Ala Val Cys	
221	740 745 750	
223	cca gcc cag tat gga atc cct gaa cca tgg aat ttc cct ttt cgg agg	2304
224	Pro Gly Gln Tyr Gly Ile Pro Glu Pro Trp Asn Phe Pro Phe Arg Arg	
225	755 760 765	
227	agc tac tgg tgt gga cct ggg cct ccc aag agt tct gtc ttg gcc cct	2352
228	Ser Tyr Trp Cys Gly Pro Gly Pro Pro Lys Ser Ser Val Leu Ala Pro	
229	770 775 780	
231	gcc cca caa gat ccc aag gtt ctg gtg gaa gag cca ccc ctt gcc ctg	2400
232	Ala Pro Gln Asp Pro Lys Val Leu Val Glu Glu Pro Pro Leu Gly Leu	
233	785 790 795 800	
235	gtt cct ggt gtc tcc att cga gcc ctg aag aaa cat ttt cgt gcc tgt	2448
236	Val Pro Gly Val Ser Ile Arg Gly Leu Lys Lys His Phe Arg Gly Cys	
237	805 810 815	
239	ccg cag cca gcc ctg caa gga ctc aac ctt gac ttc tac gaa gcc cac	2496
240	Pro Gln Pro Ala Leu Gln Gly Leu Asn Leu Asp Phe Tyr Glu Gly His	
241	820 825 830	
243	atc act gcc ttt ttg ggt cac aac ggg gct gcc aag aca acc aca ctg	2544
244	Ile Thr Ala Phe Leu Gly His Asn Gly Ala Gly Lys Thr Thr Thr Leu	
245	835 840 845	
247	tcc att ttg agt ggt ctc ttc cca ccc agt agt gcc tgc gcc tcc atc	2592
248	Ser Ile Leu Ser Gly Leu Phe Pro Pro Ser Ser Gly Ser Ala Ser Ile	
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253	865 870 875 880	
255	ggc atc tgc ccg cag tac aat gtg ctg ttt gat atg ctg aca gtg gaa	2688
256	Gly Ile Cys Pro Gln Tyr Asn Val Leu Phe Asp Met Leu Thr Val Glu	
257	885 890 895	
259	gaa cat gtt tgg ttc tat gcc cgt ttg aaa gcc gtg agt gca gcc gcc	2736
260	Glu His Val Trp Phe Tyr Gly Arg Leu Lys Gly Val Ser Ala Ala Ala	
261	900 905 910	
263	atg gcc ccc gag cgg gaa cgt ctg ata cgg gat gtg ggg ctt acc ctc	2784

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268 Lys Arg Asp Thr Gln Thr Arg His Leu Ser Gly Gly Met Gln Arg Lys
269      930          935          940
271 ctt tct gtg gcc att gcc ttt gtg ggt ggc tct cgt gtg gtc atc atg 2880
272 Leu Ser Val Ala Ile Ala Phe Val Gly Gly Ser Arg Val Val Ile Met
273 945          950          955          960
275 gac gag ccc act gct ggt gtg gac ccc gct tcc cgc cgt ggc att tgg 2928
276 Asp Glu Pro Thr Ala Gly Val Asp Pro Ala Ser Arg Arg Gly Ile Trp
277          965          970          975
279 gaa ttg cta ctt aag tac aga gaa ggt cgg aca ctg att ctc tcc act 2976
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283 cac cac ctg gat gag gca gag ctc ttg gga gat cgc gtg gcc atg gtg 3024
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285          995          1000          1005
287 gca ggt ggc tct ttg tgc tgc tgt ggg tcc ccg ctt ttc ttg cgc cga 3072
288 Ala Gly Gly Ser Leu Cys Cys Cys Gly Ser Pro Leu Phe Leu Arg Arg
289      1010          1015          1020
291 cac ttg ggc tgc ggt tac tac ctg acc ctg gtg aag agt tct cag tcc 3120
292 His Leu Gly Cys Gly Tyr Tyr Leu Thr Leu Val Lys Ser Ser Gln Ser
293 1025          1030          1035          1040
295 ctc gtc acc cat gat gct aag gga gac agt gag gac ccc aga cgg gaa 3168
296 Leu Val Thr His Asp Ala Lys Gly Asp Ser Glu Asp Pro Arg Arg Glu
297          1045          1050          1055
299 aag aag tca gat ggc aat ggc agg acg tca gac aca gcg ttc aca cga 3216
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301          1060          1065          1070
303 gga acc tca gac aag agc aac cag gcc ccg gct cct ggc gcc gtt ccc 3264
304 Gly Thr Ser Asp Lys Ser Asn Gln Ala Pro Ala Pro Gly Ala Val Pro
305          1075          1080          1085
307 atc acc cca agc aca gcc cgg ata cta gag cta gtg cag cag cat gtg 3312
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311 cct gga gca caa ctc gtg gag gac ctg ccc cat gag ctt ctg ctt gtg 3360
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313 1105          1110          1115          1120
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316 Leu Pro Tyr Ala Gly Ala Leu Asp Gly Ser Phe Ala Met Val Phe Gln
317          1125          1130          1135
319 gag ctg gat cag cag ctg gag ctc ctg ggt ctc aca ggc tac ggg atc 3456
320 Glu Leu Asp Gln Gln Leu Glu Leu Leu Gly Leu Thr Gly Tyr Gly Ile
321          1140          1145          1150
323 tcg gac acc aac ctg gag gag atc ttc cta aag gtg gtg gag gat gcg 3504
324 Ser Asp Thr Asn Leu Glu Glu Ile Phe Leu Lys Val Val Glu Asp Ala
325          1155          1160          1165
327 cac aga gaa ggt ggg gac tct aga ccg cag ctg cac ctt cgc aca tgc 3552
328 His Arg Glu Gly Gly Asp Ser Arg Pro Gln Leu His Leu Arg Thr Cys

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:3516 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9